

FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCCGCCCTTGGCGGGGCGGCCCTCCGGCTCAGGCTGGCTGAGA
 GGCTCCCAGCTGCAGCGTCCCCGCCGCCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGGC
 CTCGGGGACCAAAACAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCA
 TGATCATGGTTTACTGCGACCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA
 CTACAGGACAAAAATTAGAAATCAAAATGGAAAAATATGCTGCTTTGGTTGATATTTTTACC
 CTCGGGTGGACCTTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
 GGTACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCTTTGAGGCAGATG
 CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAAAAGCTCCCAACTCCCAGC
 CTTTCTGAATTGGAGGATTATCTTTCTATGAGACTGTCTTTGAGAATGGCACCCGAACTTT
 AACCAGGGTGAAAGTTCAAGATTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
 TATCTGTTAGGAGAAAGACAGGTGTATGGCACCGACAGCAGGTTTCAGCATCTTGGACAAA
 AGGTTCTTAACCAATTTCCCTTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
 TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCCACTGTGTTTCATGATGGAAGGACTATG
 TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAAATAAAAGTGGAGGCAAG
 AAACGTGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGTGACCAAAGAGAGGGTAC
 CAGAGAGCATCTGCGAGGAGAGAGCGAAGGGTGGGAGAGAAGAAAAAAATCTGGCCGGGGTC
 AGAGGATTGCGGAAGGGAGGCCCTTCTTTCACTGGACCCGGGTTCAAGAATACCCACATTCG
 AAGGGCTGGCGACAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA
 GCTGAAGCGTGCTCACAAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA
 TGCCTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
 CGGTTTTGCAGTGTGTCCGACGAATCCAATGATCTCTTTTACCAATACTGCGATGCTGAGTC
 GGGCTCCACCGGTTTCGGGGGTCTATCTGCGCTGAAAAGATCCAGACAAAAAGAATTGGAAGC
 GCAAAATCATTTGCGGTCTACTCAGGACCCAGTGGGTGGATGTCCACGGGGTTTCAGAAAGGAC
 TACAACGTTGCTGTTTCGCATCACTCCCTAAAAATACGCCAGATTTGGCTCTGGATTACCGG
 GAACGATGCCAATTGTGCTTACGGCTTAAAGAGACCTGAAACAGGGCGGTGATCATCTAAA
 TCACAGAGAAAAACAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCTCTGGACTT
 GAACTCTGTCAATAGCATTTCAACATTTTTCAAATCAGGAGATTTTCGTCATTTAAAAAA
 TGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA
 CATGGTGATGAGTTTCATTGTGAGAAAAATTTTGTGCTCTCTTAAAAATTAGACACACTTT
 AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATCTCAGGGTCC
 TACTCTAAGAAGAAATCTAATAGGATGCTGGTTGTGATTAAATGTGAAATTGCATAGATAAA
 GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA
 CTCTGAGATGGATCCATTGAGCTCATGCCCTCAATGTTTATATTGGTTATCTGTTGGGTCT
 GGGACATTTAGTTTAGTTTTTTTGAAGAAATTCAAAATCAGAAGAAAAAGCAAGCATTATAAA
 CAAACTTAATAACTGTTTTTACTGCTTTTAAAGAAATAACAATTCAATGTGATTATTTAAAAA
 TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTGAAGAAATAGGGAAGCTGAGACATTT
 TAAGATCTCAAGTTTATTTTAACTAATATCTAAAATATGGACTTTTCATGTATGCATAGGG
 AAGACACTTCAAAATTTAGATGATCATGTGTTGAAGGCCACATTTATTTATGCTATATCAT
 TCTATTTGATGAGGTGCTACATTTTATAGGACAAAGAAATCTGTAATCTTTTCAAGAAAGAGT
 CTTTGTCTCTCTGACAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG
 TAATTTTAGATATGCTCTTTCTCAAAATGAATAAAATTTATGAATAGA

09070205.10.1501

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253
<subunit 1 of 1, 413 aa, 1 stop
<MW: 47070, pI: 9.92, NX(S/T): 3
MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSILDKRFLTNNPFFSTAVKLSTGCSGILISPQHVLTAAHCVDGKDYVKGSKKLRV
GLLKMRNKS GKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDENDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNAVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

0973235-10453

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGAGGGGCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCACCAGAAGCAGGTGATTTCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAGGAACAACCCCTGGTTGTTGAACTAGCACCTAAGGTCCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCTTGTCTTAAAGGTCCTGATCACTT
ATATCTGGAAACCAAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCATTGTCAAGATTGTAACTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCCTTCTCGTGGGAGGCCACCCCATGGACCGCTGCTCCTCC
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGACATCCAGGGGCA
TGTCACCTCAGTGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCCAAAAAAGGCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAACTTCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGAGGAGCCCTCGTTAAGTTGTAAAAGCACAGACTGTTCTATA
TTTGAACATGTTTTGTTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAGATTGATTAGTTTCAA
AAAAA

0978295.101501